

Σ 610N0:2

Fig. 1

GS wild-type

004020-29626450

10 20 30 40 50 60 70 80 90 100 110 120

130 140 150 160 170 180 190 200 210 220 230 240

250 260 270 280 290 300 310 320 330 340 350 360

370 380 390 400 410 420 430 440 450 460 470 480

490 500 510 520 530 540 550 560 570 580 590 600

610 620 630 640 650 660 670 680 690 700 710 720

730 740 750 760 770 780 790 800 810 820 830 840

850 860 870 880 890 900 910 920 930 940 950 960

970 980 990 1000 1010 1020 1030 1040 1050 1060 1070 1080

1090 1100 1110 1120 1130 1140 1150 1160 1170 1180 1190 1200

1210 1220 1230 1240 1250 1260 1270 1280 1290 1300 1310 1320

1330 1340 1350 1360 1370 1380 1390 1400 1410 1420 1430 1440

ATGAAATA ATATTATG ATATTATG ATATTATG ATATTATG ATATTATG ATATTATG ATATTATG ATATTATG ATATTATG ATATTATG ATATTATG

CTGCAAAAT GGTGTAATG TTGAAATAA TTTTATATA ATATATGTC TGTCTTGTG TGTCTTGTG TGTCTTGTG TGTCTTGTG TGTCTTGTG TGTCTTGTG TGTCTTGTG

CCAACTGCTA CTGCTAAATTT AGTCACATAA TGTAAAGTTA ATATGCTGC ATATGCTGC ATATGCTGC ATATGCTGC ATATGCTGC ATATGCTGC ATATGCTGC ATATGCTGC

AAATTTTATA ATGAAATGC TCCAAATTTT AATGCAAGTG CTATGATATG CACAGCTGT CACAGCTGT CACAGCTGT CACAGCTGT CACAGCTGT CACAGCTGT CACAGCTGT

TGTAAAGTGC CAGTCTCTAC TGTAAAGTGC CTTGATATG GATTAATAC TGAATATG TGAATATG TGAATATG TGAATATG TGAATATG TGAATATG TGAATATG TGAATATG

AAATCTCTT TCAATCCAGG TAAAGTTAA TCCACACCTT CTGCGGCAAT TAAAGTTAA TAAAGTTAA TAAAGTTAA TAAAGTTAA TAAAGTTAA TAAAGTTAA TAAAGTTAA

TGCTCTGATG GTACTATAAG TGTCTCTGCA GTAAATATG TGAATATG TGAATATG TGAATATG TGAATATG TGAATATG TGAATATG TGAATATG TGAATATG

AGTACATGCC TACCTTGCCC AGCAATATAA GATTAATGCTG CTGACGCCAC TCCAGGTGCT TCCAGGTGCT TCCAGGTGCT TCCAGGTGCT TCCAGGTGCT TCCAGGTGCT TCCAGGTGCT

GGAGCACTA ATTAATGTAAT ATTAATAACA GAATGCTCTA ATGCTGCTGC TAACTTTTAT TTGATGCTA ATTAATCTA ATTAATCTA ATTAATCTA ATTAATCTA ATTAATCTA

GTTTAAAGCG CTGTACACAC TCCAGGTGCT ACTGCTACTT TAATTCCTA ATGCTGCTGC GATGCTGCT GATGCTGCT GATGCTGCT GATGCTGCT GATGCTGCT GATGCTGCT

TCTGATGTC TTAATGTCG TCCCACTTTT TATCTACAA ATTAATCTA TTGGGTAGA GATTAATCTA GATTAATCTA GATTAATCTA GATTAATCTA GATTAATCTA GATTAATCTA

CCGATATCG CTAAATAAAA TATATATATG GATTTGCTA ATTTTATC ATTTTATC TATTAATTT TATTAATTT TATTAATTT TATTAATTT TATTAATTT TATTAATTT TATTAATTT

Coding region: nucleotides 1-1404

Fig. 2(a)

## G5 SYNTHETIC

004020" 29626460

SE410  
NU:  
102

10	20	30	40	50	60	70	80	90	100	110	120
ATGAGAAC	ACATCTGT	GATCTGAT	ATCTCTGT	TCATCAACA	GATCAGCT	GCTAACTGT	CTGTGAGAC	ACCGCTGAC	AGCTGACGA	CCTGGAGAC	
130	140	150	160	170	180	190	200	210	220	230	240
CCTGTAAC	GTGTGATC	TCAGAGAAC	TTCTACTACA	ACAAGCTGC	TGCTTTGCT	CCTGAGCTT	CTAACTGTAC	CCCTTTGCT	CAGAGAGAG	ACGCTGAGC	TCAGCTTAC
250	260	270	280	290	300	310	320	330	340	350	360
CCCTCTGTA	CCGCTAACCT	GCTGACCCAG	TGTAACTGTA	AGTGTCTGC	TGGAACGCT	ATGCTGAG	GAGCTACCGA	CTAACCTGCT	ATCATCACCG	AGTGTGTGTA	CTGTGCTATC
370	380	390	400	410	420	430	440	450	460	470	480
AACTTCTACA	ACGAGAGGC	TCTTAATCTC	AACGCTGAG	CTTCTACTG	TACCGCTGT	CCGTGTAAC	CGCTGGAG	AGCTGTGAC	GCTGAAAG	CTGTAACAT	CGTGGCTGAG
490	500	510	520	530	540	550	560	570	580	590	600
TGTAACTG	CTTGTCTAC	CGGAACTG	CTGAGAGAG	GAGTACAC	CGACTACTG	CGCTTTTCA	CCGAGTGT	GAGTGTGCT	CTGAATCTT	ACTTAACCG	AAACACCGA
610	620	630	640	650	660	670	680	690	700	710	720
AAACACCTT	TCAACTG	AAAGTCTCAG	TGTAACTG	GTCTCTGAT	GAAGCTGCT	AAAGTGTGCT	AGGCTACCT	GGGAAACGAC	GCTAACATCA	CCGCTGAGT	TAACTGCT
730	740	750	760	770	780	790	800	810	820	830	840
TCCTGAG	GAACTCTC	TCCTCTGTA	GTAACTACT	GGTGTCTCA	GAACCTGAG	TGTAACTG	GTCTCTTAA	CTTCTACAC	AACAACTG	CTAACTTCA	CCCTGAAAC
850	860	870	880	890	900	910	920	930	940	950	960
TCTACTGTC	TGCTGTGCT	TGCTAACAG	GACTACGAG	CTGAGCTAC	CGCTGAGGA	GCTGTAAC	TGCTGAGCA	GTGTAACTG	GCTGTGCTG	ACGTAACG	TATGCTTCT
970	980	990	1000	1010	1020	1030	1040	1050	1060	1070	1080
GGAGCTACA	ACTAGTGT	CTGTAAC	GAGTGTCTCA	ACTGTGCTG	TAACTTCTAC	TTGAGAGGA	AACTTCTCA	GCTGTGATCT	TCCTGCTGTA	AGCTTGTCT	TGCTAACAG
1090	1100	1110	1120	1130	1140	1150	1160	1170	1180	1190	1200
GTGAGGAG	CTGTGCTAC	CCCTGAGGA	ACCGCTAC	TGATGCTCA	GTGTGCTG	GAGTGTGCT	CTGTAACCT	GCTGAGGAC	GGAACTGCT	CTAACTTCA	GAAGCTGCT
1210	1220	1230	1240	1250	1260	1270	1280	1290	1300	1310	1320
TCGAGTGTG	TGAAGTGTG	TGCTACTTC	TACACTTCA	AGCAGAGGA	CTGTGCTG	GGATGCTCA	CCCTGAGCT	TGTAACTG	AACTGCTG	CTGAGCTG	GGCTAACTG
1330	1340	1350	1360	1370	1380	1390	1400	1410	1420	1430	1440
CCCTGAGTGTG	CTAAGAGGA	CACTGCTGT	GACTTCTGTA	ACTTCTGCT	TACTTCTG	CTGCTGATCT	CTTACTACT	GCTGTAACTA	.....	.....	.....

Coding region: nucleotides 1-1404

Fig. 2(b)

[illegible]

SEB 10 NOV 6 61  
SEB 10 NOV 7 61

/  
 /  
 MKNNILLIILSLFINELRAVPCPDGTQT-QAG-LTDVGAADLGTVCNCRNFYNN-----  
 MKNNILVILLIILSLFINQIKSANCPUVGETNTAGQVDDLGTGP--ANCVNCQKNFYNNAA  
 \*\* \*\*\*:\*\*\*\*\*+:::.. \*\* \*\*\* \*\* \*: \*+:::.. \*\* \*\*\*: \*\*\*\*\*

51

55 --GGAA-----QGRANGQP-----  
54 FVPGASTCPCPOKKDACAQPNPPATANLVTCQNVKCPAGFALAGGATDYAAIITECVNC  
\*\* : \* \* \*

55 61

68 ---P-----AAN-NAARGICVPCQINRVGSVTNAGDLATLATQCSTCCPTGTALDDGVTDV  
119 RINFYNEAPNFENAGASTCTACPNVRUGGALTAGNAATTIVACNVACTGTGTALDDGVTTD

51 55

10 FDRSAACVCVKCKPNEFYNGGSPQGEAPGVQVFAAGAAAGVAAVTSQCVPCQLNK--NDS  
11 YVRSFTEVCVKCRLNFYNGNN--GNTP-----FNPGK-----SCTPCPAIKPANVA  
: \*\*::\*\*\*\*\*:\*\*\*\*\*): \*\*:: \*\* \* \* \* \* \*

51 55

16 PATAGAQANLATQCSNQCPTGTVLDDGVTLVNTSATLCVKCRPNFYNGGSPQGEAPGV  
 24 QATLGNDATITACQNVACPDGTISAAGVN--NWVAQNTCTNCAPNFTNN-----AP--  
 \*\* \* : \* : : \* \* \* \* \* \*\* \* \* : : \* \* : \* \* \* \* \* \* \*

51

8 QVFAAGAAAGVAAVTSQVPCINKND-SPATAGAQAQLATQCSNQCPCTGTAIQDGVTL  
5 -NTNPG-----NSTCLPCPANKDYGAETAGGAATLAKQCNIACPDGTALASGATN

15

47 VFSNSSTQCSQCIANYFFENG-NFEAGKSQCLKCPVSKTTPAHAP-GNTATQTXQCLTTCP-  
 5 -XVILQTECLNCAANFYEDWNFNQAGSSRCKACPANKVQGVATAGGTATLTAQCALECP  
 : \*:\*

15

AGTVLDDGHSINNFVASATFCTKCSAGFASKITGTAGTDTCTECTKKLTSGATAKXVYAE  
AGTVLTGQHTSTYKQAASECVKCAANFYTKQTDDWAGIDTCTSCNKKLTSGAENLPES  
\*\*\*\*\* \*\*::: :\*: \*\* \*\*\*: \*::: \*::: \*\* \*\* \*\* \* \*\*\*\*\* \*\*..

110

\* : : \*  
ATQKVQCSTFAKFLSLSLLFISYLL  
AKNNIQD--PANFLSLSLLLISYLL  
\*\*\*\*\*

Fig. 3(a)

Seq ID

90 MKYNILILISLFIN  
91 MKNNILVILISLFIN

97 CPTGTHLDDGVT

93 CVKCKPNFY YNG  
94 CVKCKLNFY YNG

95 C P A G T V L D D G T  
96 C P A G T V L T D G T

97 AGTDTC TECTKK LTS6AA  
98 AGFDTC TSCNKK LTS6AE

99 FAKFLSISLLFISFYLL  
100 FANFLSISLLISYLL

[illegible]

GTTCCAGTCTCTGATGGTACTTAGACTCA-----AGCTGGAT-----TGACTGATGTAGGTGC  
 GCTAATTGTCTCTGTTCGAAGCTGAAGCTAACACAGCCGATTAAGTTCA-TGATCTAGGAAC  
 \* \* \* \* \*  
 TCGTGAATCTTCGACTTGTGTTAATTGC-AGACCTAATTTTACTATAATGTTGTGCTG  
 TCCT-----GCATAATGTGTTAATTGTTAGAAA-AACTTTTATTATAAATGCTGCTG  
 \* \* \* \* \*  
 CTTAAGGAGAAGCTAATGGTAATTAACCTTTGCGAGCAAAATAAGTCTGCTAGAGGTAAAT  
 CTT-----TCGTTC-----TGGTGCTAG-----TACGT  
 \* \* \* \* \*  
 GTGTACCATTG-CCA-AATAAACAGA-GTAGGCTCTGTTACCAA-TGCAGGTG--ACTTAG  
 GTACACCTTGTCCATAAAAAAAGATGCTGTCT-TAACCAATCCACCTGTACT--G  
 \* \* \* \* \*  
 CTACTTTAGCCACATAATGCGACTTAAATOTCTACTGGCACTGCACTTGATGATGGAG  
 CTAATTAGTCAATAAGCTTAAATGCGCTGCTGGTAGCCCAATTGCAAGGTGAG  
 \* \* \* \* \*  
 TGACAGATGTTTGTG--ATAGATCAGCCGCATAATGTTTAAATGCAAACTTAACTTTAA  
 CAACAGATTATGCAAGCAATA-ATCA-----CAGAATGTGTTAATTGAGAATTAAATTTTAA  
 \* \* \* \* \*  
 CTATAATGOTGGTTCTCTTAAAGTGAAGCTCTGGCGTTTAAAGTTTGTGCTGCTGGTGC  
 --TAATGA-----AA-----ATGCTCC-----AAATTTTAA-----  
 \* \* \* \* \*  
 TGGCGGTGCAAGGTGTTGCTGCCGTACTACTTAATGTGTACCTGCCAACTAAACAAAAA  
 -----TGCAGGTG-----CTAGTACATGACACAGCTTTGTCCGGTAAACAGAGT  
 \* \* \* \* \*  
 CGATTCTCTGCCACTGCGAGGT---GCCTAAAGCTAATTAGCCACATAATGTAGCAATTA  
 TGGTGGTGCATTGACTGCTGTGTAATGCC---GCTACCAAGTCCGATAATGTAAAGTCCG  
 \* \* \* \* \*

Fig. 3(b)

G1 ATGTCTACTGGCACTGTACTTGATGATGGAGTGACACTTGTTTTAAATACATCAGCCAC  
G5 ATGTCTACTGGTACTGCACTTGATGATGGAGTAACTACTGATTATGTTAGATCAATTCAC  
.....

G1 ATTATGTGTTAAATGCAGACCTAACTTTTACTATAATGGT-----GGTT---CTCCCTA  
G5 AGAATGTGTTAAATGTAGACTTAACTTTTACTATAATGGTAAATAATGGTAATACTCCCTT  
.....

G1 -----AGGTGAA-----GCTCCTGGGGTTTA  
G5 CAATCCAGGTAAGTAAATGCACACCTTGTCCGCAATTAACCTGCTAATGTTCTTA  
.....

G1 AG-----TTT-----TTGC-----TGCTGG  
G5 AGCTACTTACGTAATGATGCTACAATAACCGCATATGTAACGTTCATGCCCTGATGG  
.. ..

G1 TGCT-----GCCGCTGCAG-----GTGTTGC-----  
G5 TACTATAAGTCTGCTGAGTAAATTAATGGGTAGCACAAACACTGAATGTACTAATTG  
.. ..

G1 -----TGCCCTTACTAGTTAATGRT  
G5 TGCTCCTAACTTTTACAATAAATGCTCCTAATTTCAATCCAGGTAATAGTACATGCCCT  
.. ..

G1 ACCCTGCCAAATAAACAACAAACGATTCTCTG---CCACTGCAGGTGCCTAAGCTAATTT  
G5 ACCTTGCCCAAGCAATAAAGATTATGGTGTGAAGCCACTGCAGGTGGTGGCGCTACTTT  
\*\*\*\*\* \* ..

G1 AGCCACATAATGCAGTACTTAAATGTCCAACCTGGCACTGCAATT-CAAGACGGAGTGCAC  
G5 AGCCAAATAATGTAATATGCTATGCCCTGATGGTACTGCAATTGCTAGT-GGAGCAAC--  
\*\*\*\*\* ..

G1 TTGTTTTAGTAAT-TCATCCACATAATGTTCTTAAT-GCATTGCTAATTACTTTTTAA  
G5 -TAATTAT-GTAATATTATAACAGAAATGT-CTAAATTGTGCTGCTAACTTTATTTTGA  
\* ..

G1 TGGTAAT---TTCAAGCAGGTAAAGTTAATGTTTAAAG---TGTCCAGTAAATAAACT  
G5 TGGTAATAATTTCTAGGCAGGAAGTAGTAGATCC--AAAGCATCTCCAGCAATAAAGTT  
\*\*\*\*\* ..

G1 A-----CTCCAGCACATGCTCCAGGTAATGCTACTTAAAGCCACATAATGT---TT  
G5 TAAGGCGCTGTAGCAA---CTGCAGGTGGTACTGCTACTTTAATTGCATAATGTGCCCTT  
.. ..

G1 GACCACATGTCCTGCTGGTACAGTACTTGATGATGGAACATCACTAATTTGTAGCTTC  
G5 GA-----ATGCCCTGCTGGTACTGTACTCACCAGTGAACAACATCTACTTATAAATAAGC  
.. ..

G1 CGCAACTGAATGTACTAAATGTTCTGCTGGCTTTTTCATCAAAAAACACTGCTTTTAC  
G5 AGCATCTGAATGTGTTAAATGTGCTGCCAAGTTTATCTACAAAATAAAGTATTGGGT  
.....

G1 ACCAGGTACTGATACATGTACTGAATGTACTAAAAAATTAACCTTCTGGTGCCACAGCTAA  
G5 AGCAGGTATTGATACATGCTAGTTGTAATAAAAATTAACCTTCTGGCTGAAGCTAA  
\*\*\*\*\* ..

G1 AGTATATGCTCAAGCTACTCAAAAAG---TATAATGCGCTCCACTACTTTTCGCTAAAT  
G5 TTTAC---CTGAATCTGCTAAAAAATATATAATGTG-----ATTTCCTAATTT  
.. ..

G1 TTTATCGATTTCCTATTATTATTCTTTCTATTATTG  
G5 TTTATCAATTTCTATTATTATTCTTTATTATTATTA  
\*\*\*\*\* ..

Fig 3(b)  
(cont)

# 65 kD i-antigen protein

10 20 30 40 50 60  
 EG 1040:7 MKNILVILI ISLFINQIKS ANCPVGTETN TAGQVDDLGT PANCVNCQKN FYNNNAAFV  
 70 80 90 100 110 120  
 PGASTCTPCP QKRDAGAQP N PPATANLVTO CNVKCPAGTA IAGGATDYAA IITECVNCRI  
 130 140 150 160 170 180  
 NFYNENAPNF NAGASTCTAC FVNRVGGALT AGNAATIVAQ CNVACPTGTA LDDGVTTDYV  
 190 200 210 220 230 240  
 RSFTECVKCR LNFYYNGNNG NTPFNPGKSQ CTPCPAIPKA NVAQATLGND ATITAQC NVA  
 250 260 270 280 290 300  
 CPDGTISAAG VNNWVAQNT E CTNCAPNFYN NNAPNFNPGN STCLPCPANK DYGAETAGG  
 310 320 330 340 350 360  
 AATLAKQCNI ACPDGTALAS GATNYVILQT ECLNCAANFY FDGNNFQAGS SRCKACPANK  
 370 380 390 400 410 420  
 VQGAVATAGG TATLIAQCAL ECPAGTVLTD GTTSTYKQAA SECVKCAANF YTTKQTDWVA  
 430 440 450 460 470 480  
 GIDTCTSCNK KLTSGAEANL PESAKKNIQC DFANFLSISL LLISYLL\*\* .....

Fig. 4

004000 29626400

# 48 kDa G1 i-antigen repeats

SEQ ID NO:

	10	20	30	40	50	60	70	80	90	
8	CPDSTOTQNS	ITDVLAAADLG	TCVSLRPNEY	YEGGAOGEA	NGNLEFAPEN	AAKII	CVPCQSERV	GVVIRAGOLA	ELATQCST	Q
9	CPTGTALDDG	VITVIDESAA	QCVKCRPEY	YNGGSEGEA	FGVVFANGA	AAAGVAAVTS	QCVPCLERN	DSPATAGACA	ELATQCES	Q
10	CPTGTALDDG	VITVFTSAT	LCVKCRPEY	YNGGSEGEA	FGVVFANGA	AAAGVAAVTS	QCVPCLERN	DSPATAGACA	ELATQCST	Q
11	CPTGTALDDG	VITVFTSAT	QCSQLANF	ANGF	FEA	GR	SQCICFVST	TPAAGET	ATCATOCT	T
12	CPAETVIDDG	TSTNEVMSAT	ELKCSACEF	ASKTTG	FTA	GTD	TCIECTKLT	SLATAKVMA	EATOKVOCAS	T

\* \* \* \* \*

Fig. 5(a)

004020-29626160



# 55 kDa G5 i-antigen repeats

Seq 10 no.	55	1	CPVGTETNTAGQVDDLGTPANCVNCQKVFYVNNAA	AFVPGFSTCTPCPKKDA	GAQPNPPAT	NLVT	QCNVK
	56	2	CPAGTAAAGG-AIDYAAIITECVNCRINFYNAP	NFNAGASTCTACHVNRVGGAL	TAGNAATIV	--	AQCNTVA
	57	3	CPTGTALDDGVITIDYVRSFITECVRQRINFVYVNGNNTBFNPGKSGCTPCPAIKPANVAQAATLGNDATITTAQCNVA				
	58	4	CPDGTLSAAGVNNWVAQN-TECTNCAAPNFYVNNAP	NFNPGNSTQPCPANKDYGAFA	TACGAATLAK	-	QCNTFA
	59	5	CPDGTALASGAFTNYVILQ-TECLNCAANFYFDGN	NFQAGSSRCKAC	PANKVQEA	APAGGIVATLI	-AQCALLE
	60	6	CPAGTTLTDGTHSTYKQAASECVKCAANFYITTKQ	TDWVAGIDICTSCNKKL	TSGAFANLPESAKKNI	-	QCDFIA

Fig. 5(b)

004020-9626460

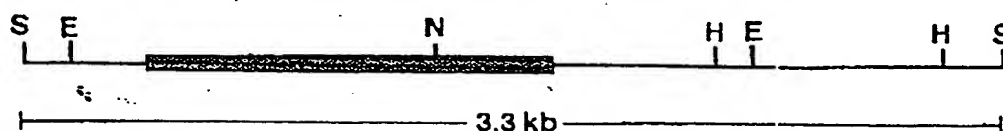


Fig. 6

Diagram illustrating the G1 isolate genome organization. The cDNA sequence is 1185 nt long, starting with an ATG start codon and ending with a TGA stop codon. The GENE sequence is 1925 nt long, also starting with an ATG start codon and ending with a TGA stop codon. A small arrow indicates a specific site within the GENE. A large arrow points from the GENE to the text "48 kDa antigen (G1 isolate)".

[illegible]

Fig. 7

20 AVFPDGTQTOAG-LTDVGAADIGTCNCRPNFYNGNAQG---ZANGNQP-FAANNAAR--GICUP---CQINRVGSVTNAGDLAT  
S'c'q 10 uoi 61 i-ag  
61 AVDCQ-----GSAGYTTDDSEVDACCKCNAPCTACAGTADKCTKCDAAGAAPYLKKTNPSPDTGTCVSAVDCQG-SAGYTT--DDSVED  
S'c'q 10 nuu v 2 vs pA6-s1

i - a g  
v b p a 6 - S 1

i-ag  
v8pA6-S1

i-ag  
vspA6-S1

i-ag VLDGTSNFVASATECINCRAGFF-----ASKTTGFT----AGTD-TQVCTKCLTSCATKVV---ABATOKVCCASTTAX 428  
vwpA6-S1 NCADGGQTDVGGKFKYCACCKDGYAPIDGICTAFAAGRTNVCTAADGTCVTCAGBYT-LMSGCGXGVAKLPGBWICLASNEX 459

File 00

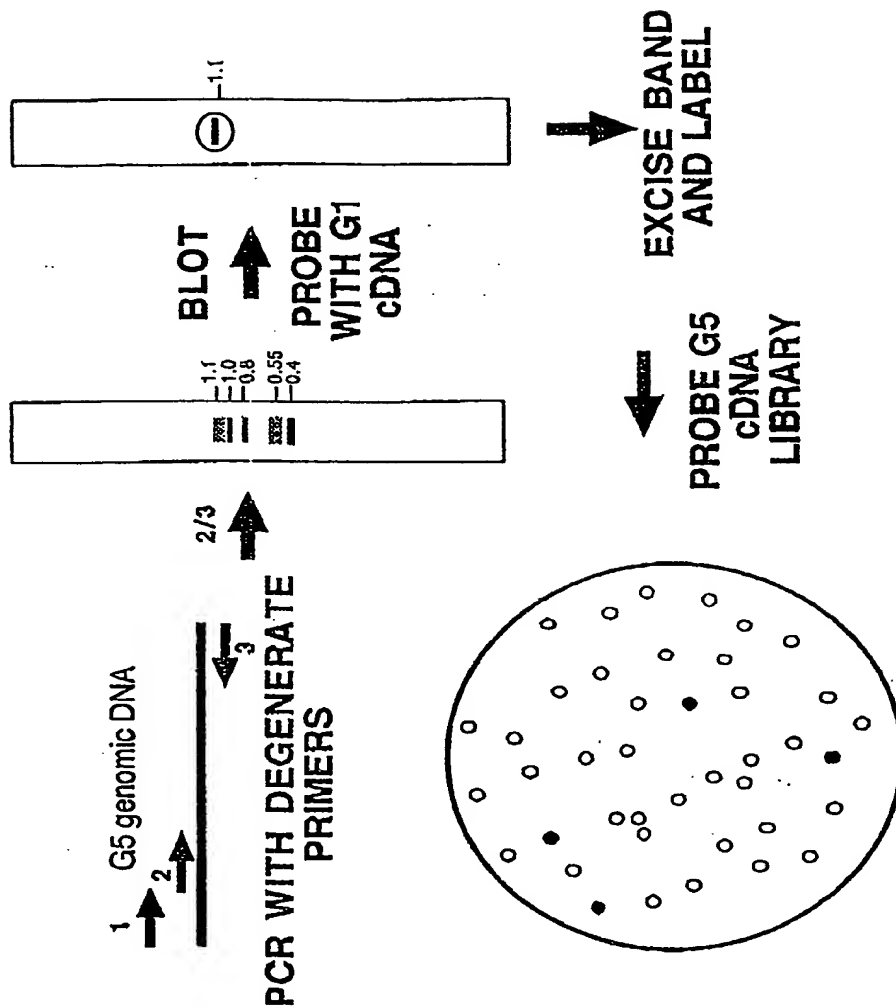


Fig. 9

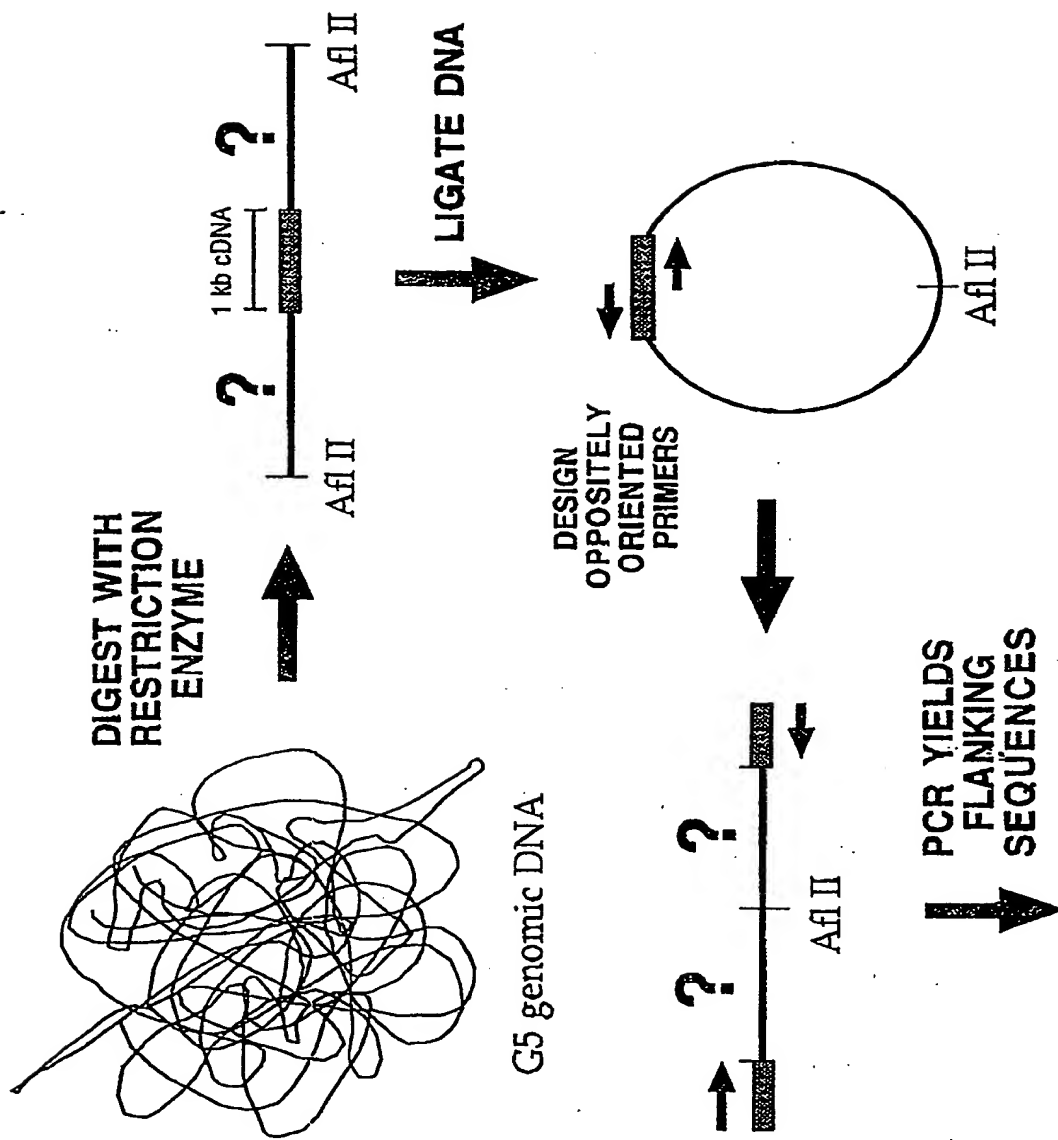


Fig. 10

004020-29626460

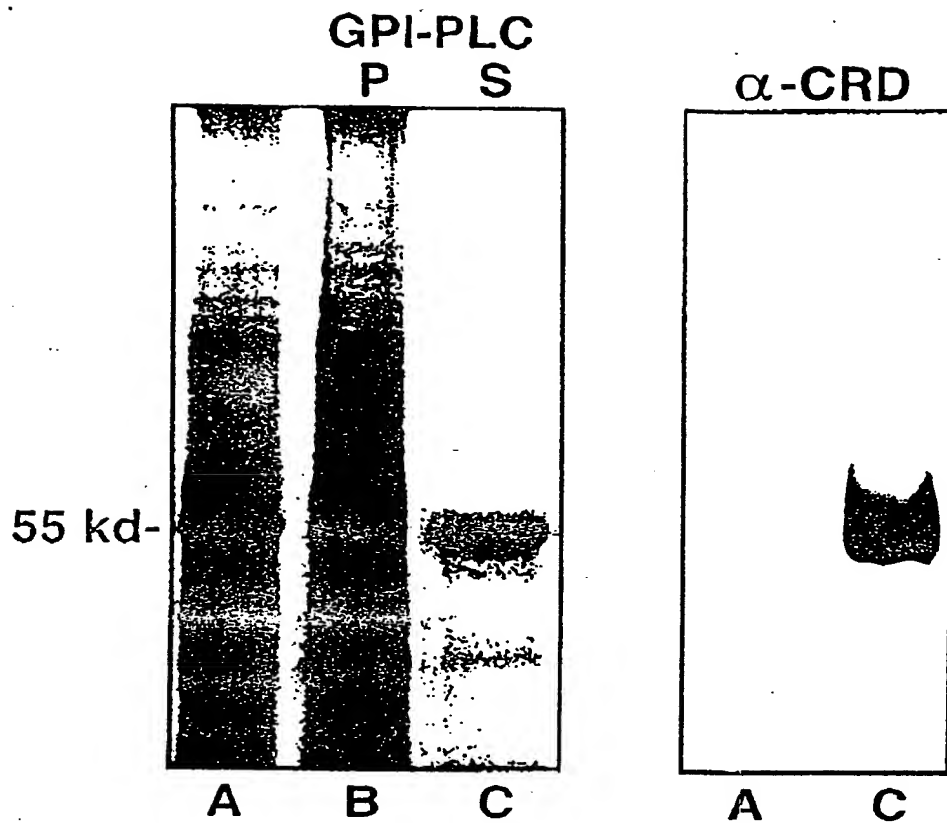


Fig. 11

SEB 10 Primers for synthesis of G5 synthetic gene.

- NO 5
- 70 3201:  
ATG GGA ATT CAA ATG AAG AAC AAC ATC CTG GTG ATC CTG ATC ATC TCT CTG TTC ATC AAC CAG ATC AAG  
TCT GCT AAC TGT CCT GTG GGA ACC GAG ACC AAC ACC GCT GGA CAG GTG
- 71 3202:  
CTC CAG GCA CGA AAG CAG CAG CGT TGT TGT AGT AGA AGT TCT TCT GAC AGT TCA CAC AGT TAG CAG GGG  
TTC CCA GGT CGT CCA CCT GTC CAG CGG TGT TGG TC
- 72 3203:  
CGC TGC TGC TTT CGT GCC TGG AGC TTC TAC CTG TAC CCC TTG TCC TCA GAA GAA GGA CGC TGG AGC TCA  
GCC TAA CCC TCC TGC TAC CGC TAA CCT GGT G
- 73 3204:  
GAT GAT AGC AGC GTA GTC GGT AGC TCC TCC AGC GAT AGC GGT TCC AGC AGG ACA CTT CAC GTT ACA CTG  
GGT CAC CAG GTT AGC GGT AGC AGG AG
- 74 3205:  
GCT ACC GAC TAC GCT GCT ATC ATC ACC GAG TGT GTG AAC TGT CGC ATC AAC TTC TAC AAC GAG AAC GCT  
CCT AAC TTC AAC GCT GGA GCT TCT ACC TGT ACC GCT TGT CCT GTG AAC CGC GTG GGA GGA GCT CTG ACC
- 75 3206:  
GGT GAA AGA GCG CAC GTA GTC GGT GGT CAC TCC GTC GTC CAG AGC GGT TCC GGT AGG ACA AGC CAC GTT  
ACA CTG AGC CAC GAT GGT AGC AGC GTT TCC AGC GGT CAG AGC TCC TCC CAC GCG
- 76 3207:  
GAC TAC GTG CGC TCT TTC ACC GAG TGT GTG AAG TGT CGC CTG AAC TTC TAC TAC AAC GGA AAC AAC GGA  
AAC ACC CCT TTC AAC CCT GGA AAG TCT CAG
- 77 3208:  
GTG ATG GTA GCG TCG TTT CCC AGG GTA GCC TGA GCC ACG TTA GCA GGC TTG ATA GCA GGA CAA GGG GTA  
CAC TGA GAC TTT CCA GGG TTG AAA G
- 78 3209:  
GGG AAA CGA CGC TAC CAT CAC CGC TCA GTG TAA CGT GGC TTG TCC TGA CGG AAC CAT CTC TGC TGC TGG  
AGT GAA CAA CTG GGT GGC TCA GAA C
- 79 3210:  
CAG ACA GGT AGA GTT TCC AGG GTT GAA GTT AGG AGC GTT GTT GTT GTA GAA GTT AGG AGC ACA GTT GGT  
ACA CTC GGT GTT CTG AGC CAC CCA GTT GTT C
- 80 3211:  
CCC TGG AAA CTC TAC CTG TCT GCC TTG TCC TGC TAA CAA GGA CTA CGG AGC TGA GGC TAC CGC TGG AGG  
AGC TGC TAC CCT GGC TAA GC
- 81 3212:  
GGT CTG CAG GAT CAC GTA GTT GGT AGC TCC AGA AGC GAT AGC GGT TCC GTC AGG ACA AGC GAT GTT ACA  
CTG CTT AGC CAG GGT AGC AGC
- 82 3213:  
CAA CTA CGT GAT CCT GCA GAC CGA GTG TCT GAA CTG TGC TGC TAA CTT CTA CTT CGA CGG AAA CAA CTT  
CCA GGC TGG ATC TTC TCG CTG TAA GG
- 83 3214:  
GAG CGA TCA GGG TAG CGG TTC CTC CAG CGG TAG CCA CAG CTC CCT GCA CCT TGT TAG CAG GAC AAG CCT  
TAC AGC GAG AAG ATC CAG CCT GG
- 84 3215:  
GAA CCG CTA CCC TGA TCG CTC AGT GTG CTC TGG AGT GTC CTG CTG GAA CCG TGC TGA CCG ACG GAA CCA  
CCT CTA CCT ACA AGC AGG CTG CTT C
- 85 3216:  
GGT GTC GAT TCC AGC CAC CCA GTC GGT CTG CTT GGT GGT GTA GAA GTT AGC AGC ACA CTT CAC ACA CTC  
AGA AGC AGC CTG CTT GTA GGT AG
- 86 3217:  
GGG TGG CTG GAA TCG ACA CCT GTA CCT CTT GTA ACA AGA AGC TGA CCT CTG GAG CTG AGG CTA ACC TGC  
CTG AGT CTG CTA AGA AGA ACA TC
- 87 3218:  
GAG GGA TCC TTA TTA CAG CAG GTA GTA AGA GAT CAG CAG CAG AGA GAT AGA CAG GAA GTT AGC GAA GTC  
ACA CTG GAT GTT CTT CTT AGC AGA CT

Fig. 12



G5 proline mutant

Seq ID  
NO:53

10	↓ 20	30	40	50	60
ATGAAGAACA	ACATCCCCGT	GATCCTGATC	ATCTCTCTGT	TCATCAACCA	GATCAAGTCT
70	80	90	100	110	120
GCTAACTGTC	CTGTGGGAAC	CGAGACCAAC	ACCGCTGGAC	AGGTGGACGA	CCTGGGAACC
130	140	150	160	170	180
CCTGCTAACT	GTGTGAACTG	TCAGAAGAAC	TTCTACTACA	ACAACGCTGC	TGCTTTCTGT
190	200	210	220	230	240
CCTGGAGCTT	CTACCTGTAC	CCCTTGTCCT	CAGAAGAAGG	ACGCTGGAGC	TCAGCCTAAC
250	260	270	280	290	300
CCTCCTGCTA	CCGCTAACCT	GGTGACCCAG	TGTAACGTGA	AGTGTCTCTG	TGGAACCGCT
310	320	330	340	350	360
ATCGCTGGAG	GAGCTACCGA	CTACGCTGCT	ATCATCACCG	AGTGTGTGAA	CTGTCCGCATC
370	380	390	400	410	420
AACTTCTACA	ACGAGAACGC	TCCTAACTTC	AACGCTGGAG	CTTCTACCTG	TACCGCTTGT
430	440	450	460	470	480
CCTGTGAACC	GTGTGGGAGG	AGCTCTGACC	GCTGGAAACG	CTGCTACCAT	CGTGGCTCAG
490	500	510	520	530	540
TGTAACGTGG	CTTGTCCTAC	CGGAACCGCT	CTGGACGACG	GAGTGACCAC	CGACTACGTG
550	560	570	580	590	600
CGCTCTTTCA	CCGAGTGTGT	GAAGTGTGCG	CTGAACCTTCT	ACTACAACGG	AAACAACGGA
610	620	630	640	650	660
AACACCCCTT	TCAACCCCTG	AAAGTCTCAG	TGTACCCCTT	GTCTCTGCTAT	CAAGCCTGCT
670	680	690	700	710	720
AACGTGGCTC	AGGCTACCCCT	GGGAAACGAC	GCTACCATCA	CCGCTCAGTG	TAACGTGGCT
730	740	750	760	770	780
TGTCCTGACG	GAACCATCTC	TGCTGCTGGA	GTGAACAACCT	GGGTGGCTCA	GAACACCGAG
790	800	810	820	830	840
TGTACCAACT	GTGCTCCTAA	CTTCTACAAC	AACAACGCTC	CTAACTTCAA	CCCTGGAAAC
850	860	870	880	890	900
TCTACCTGTC	TGCCTTGTC	TGCTAACAAAG	GACTACGGAG	CTGAGGCTAC	CGCTGGAGGA
910	920	930	940	950	960
GCTGCTACCC	TGGCTAAGCA	GTGTAACATC	GCTTGTCCTG	ACGGAACCGC	TATCGCTTCT
970	980	990	1000	1010	1020
GGAGCTACCA	ACTACGTGAT	CCTGCAGACC	GAGTGTCTGA	ACTGTGCTGC	TAACTTCTAC
1030	1040	1050	1060	1070	1080
TTCGACGGAA	ACAACCTCCA	GGCTGGATCT	TCTCGCTGTA	AGGCTTGTCC	TGCTAACAAAG
1090	1100	1110	1120	1130	1140
GTGCAGGGAG	CTGTGGCTAC	CGCTGGAGGA	ACCGCTACCC	TGATCGCTCA	GTGTGCTCTG
1150	1160	1170	1180	1190	1200
GAGTGTCTCTG	CTGGAACCGT	GCTGACCGAC	GGAACCACTT	CTACCTACAA	GCAGGCTGCT
1210	1220	1230	1240	1250	1260
TCTGAGTGTG	TGAAGTGTGC	TGCTAACTTC	TACACCACCA	AGCAGACCGA	CTGGGTGGCT

Fig. 13

proline mutant

1270	1280	1290	1300	1310	1320
GGAATCGACA	CCTGTACCTC	TTGTAACAAG	AAGCTGACCT	CTGGAGCTGA	GGCTAACCTG
1330	1340	1350	1360	1370	1380
CCTGAGTCTG	CTAAGAAGAA	CATCCAGTGT	GACTTCGCTA	ACTTCCTGTC	TATCTCTCTG
1390	1400	1410	1420	1430	1440
CTGCTGATCT	CTTACTACCT	GCTG.....	.....	.....	.....

Fig 13 (cont'd)

004020 23626460

G5 proline mutant protein

Seq ID  
No. 54

↓ 10 20 30 40 50 60

MKNNIPVILI ISLFINQIKS ANCPVGTETN TAGQVDDLGT PANCVNCQKN FYYNNAAAFV

70 80 90 100 110 120

PGASTCTPCP QKKDAGAQP N PPATANLVITQ CNVKCPAGTA IAGGATDYAA IITECVNCRI

130 140 150 160 170 180

NFYNENAPNF NAGASTCTAC FVNRVGGALT AGNAATIVAQ CNVACPTGTA LDDGVTTDYV

190 200 210 220 230 240

RSFTECVKCR LNFYNGNNG NTFPNPGKSQ CTPCPAIPKA NVAQATLGND ATITAQCINVA

250 260 270 280 290 300

CPDGTISAAG VNNWVAQNTE CTNCAPNFYN NNAPNFNPGN STCLPCPANK DYGAETATAGG

310 320 330 340 350 360

AATLAKQCNI ACPDGTALAS GATNYVILQT ECLNCAANFY FDGNNFQAGS SRCKACPANK

370 380 390 400 410 420

VQGAVATAGG TATLIAQCAL ECPAGTVLTD GTTSTYKQAA SECVKCAANF YTTKQTDWVA

430 440 450 460 470 480

GIDTCTSCNK KLTSGAEANL PESAKKNIQC DFANFLSISL LLISYVLL.. ..

Fig. 14

004020 29626460

004020" 29626460

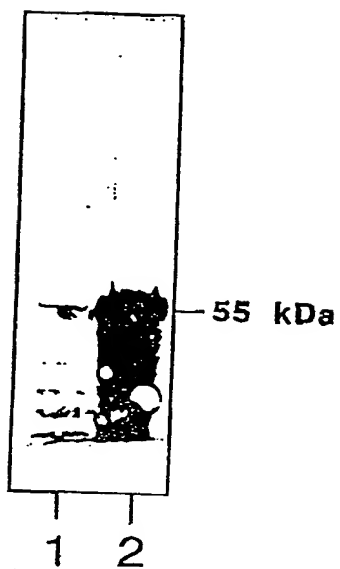


Fig. 15

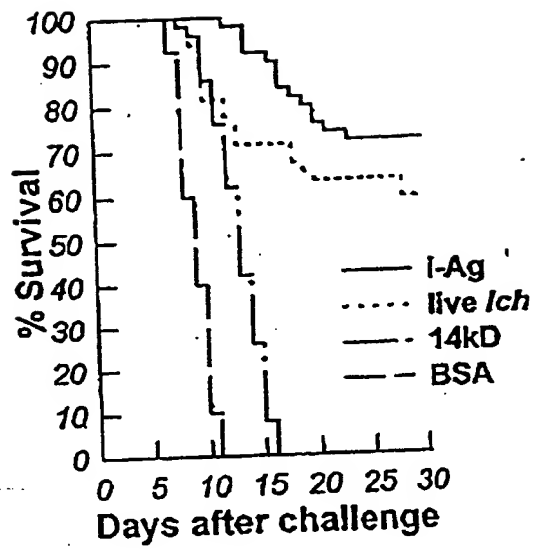


Fig. 14

004020" 29626460

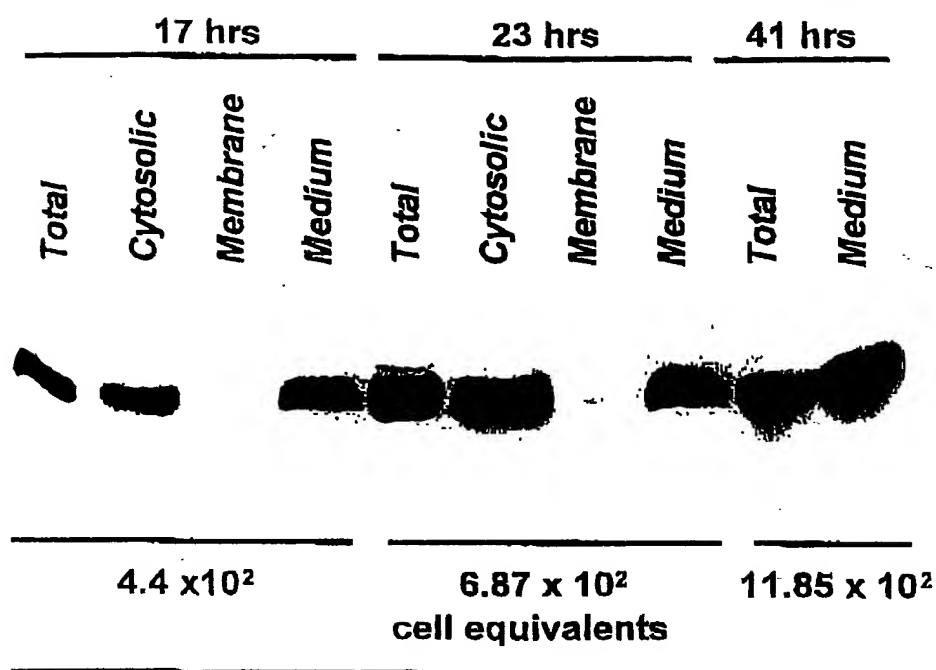


Fig. 17

004020" 29626460

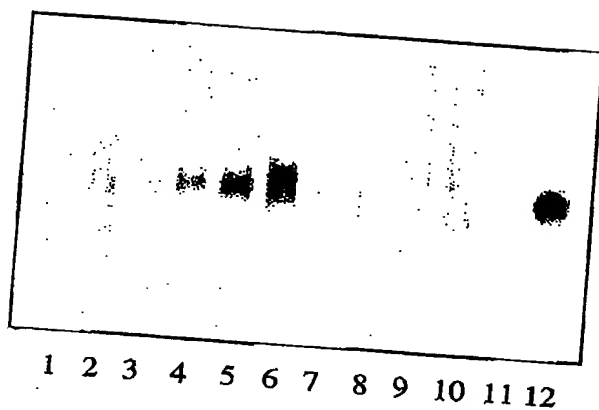


Fig. 18

000000-29626760

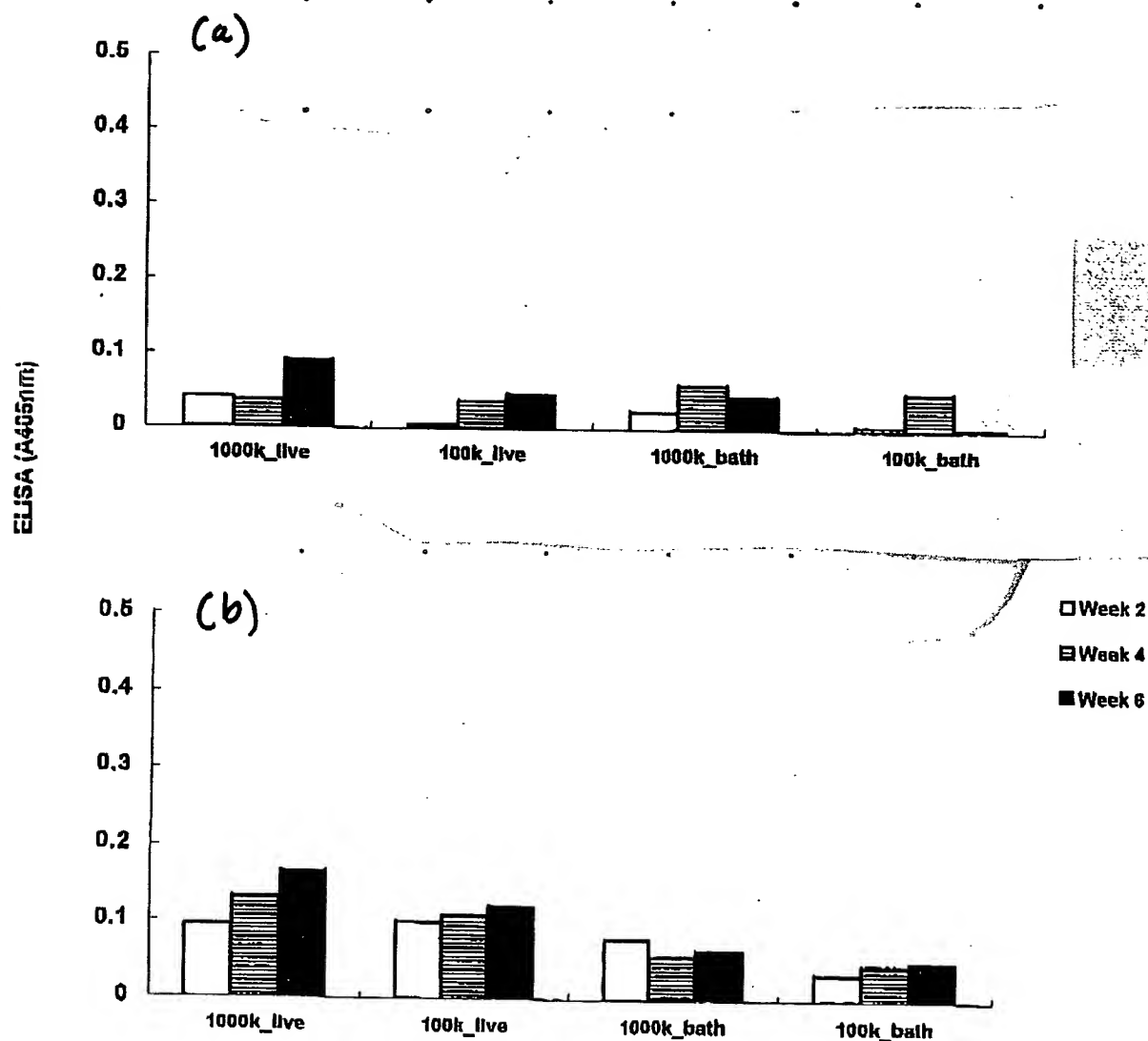
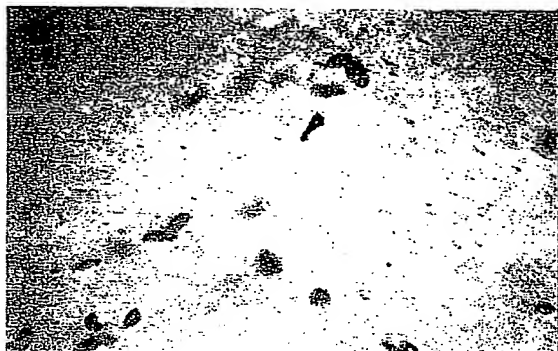


Fig. 19

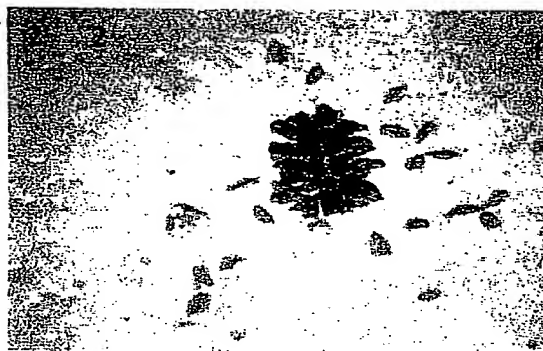


(a)



Serum: anti-live Tneo (1 : 20)  
(negative control)

(b)



Serum: anti-live TG1 (1 : 20)

Fig. 20

004020-29626460

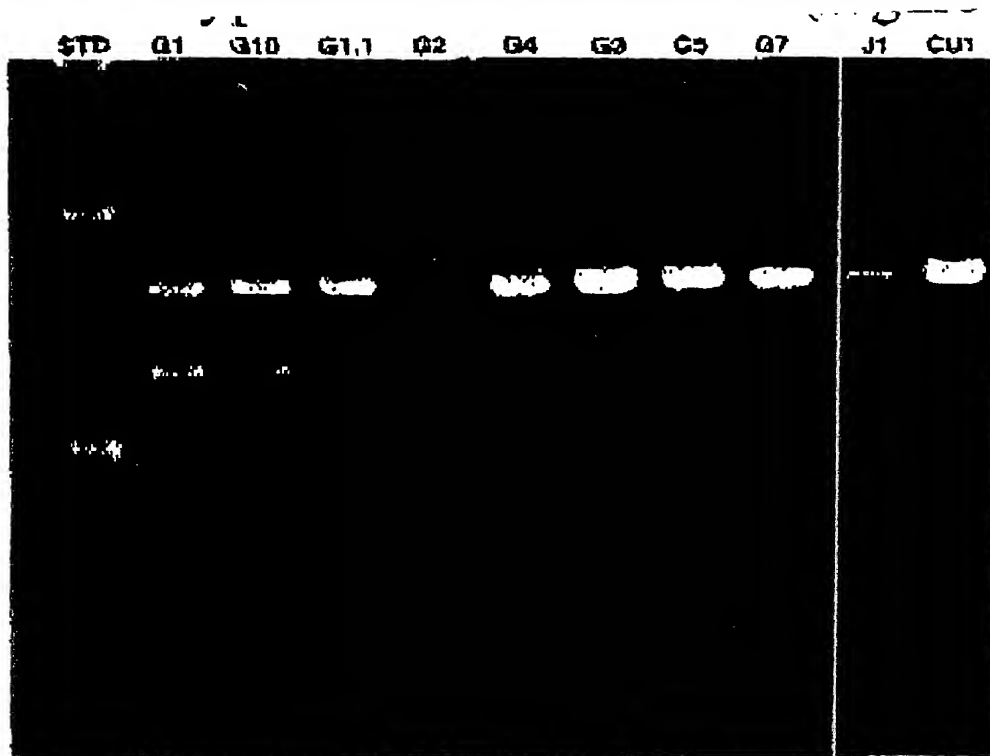


Fig. 21